

Nucleotide

Alphabet of Life

“Exhibit A”

Display Settings: GenBank

Gm1 promoter and use thereof

GenBank DD249890.1

FASTA Graphics

Comment Features Sequence

LOCUS DD249890 3871 bp DNA linear PAT 18-MAY-2006
 DEFINITION Gm1 promoter and use thereof.
 ACCESSION DD249890
 VERSION DD249890.1 GI:99025749 ← identical to SEQ ID No; 1 of 10/593,216
 KEYWORDS WO 2005108574-A/1.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus; Mus.
 REFERENCE 1 (bases 1 to 3871)
 AUTHORS Oeda,K. and Takahashi,Y.
 TITLE Gm1 promoter and use thereof
 JOURNAL Patent: WO 2005108574-A 1 17-NOV-2005;
 SUMITOMO CHEMICAL COMPANY LIMITED
 COMMENT OS Mouse
 PN WO 2005108574-A/1
 PD 17-NOV-2005
 PF 15-MAR-2005 WO 2005JP005077
 PR 15-MAR-2004 JP 04P 072244
 PI kenji oeda,yasuhiko takahashi
 CC
 FH Key Location/Qualifiers.
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

ORIGIN

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Gm1 promoter and use thereof - Nucleotide result

2/2 ページ

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//

(1)

P.

GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2009, 05:20:38 ; Search time 3986 Seconds
 (without alignments)
 98157.397 Million cell updates/sec

Title: US-10-593-216-1
 Perfect score: 3871
 Sequence: 1 gctagcccaatataatat.....gctcgaggcgagctc 3871

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 87455243 seqs, 50535937365 residues

Total number of hits satisfying chosen parameters: 174910486

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: gb_est2:
 3: gb_est3:
 4: gb_est4:
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SUMMARIES

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c 4	364.4	9.4	755	26	DH617701	DH617701	Rattus no
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c 6	260	6.7	472	2	AW494798	AW494798	UI-M-BH3-
c 7	182.4	4.7	719	5	BU709003	BU709003	UI-M-EW0-
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c 11	179	4.6	893	26	CR196564	CR196564 Forward s
c 12	177.6	4.6	652	20	AZ461261	AZ461261 1M0267K06
c 13	176.6	4.6	445	26	EF907283	EF907283 Mus muscu
c 14	176.2	4.6	584	26	CR207502	CR207502 Reverse s
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c 22	170.6	4.4	775	26	CR158875	CR158875 Forward s
c 23	169	4.4	857	26	CR239316	CR239316 Forward s
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c 26	165.8	4.3	823	20	BH040357	BH040357 RPCI-24-3
27	164	4.2	949	26	CR257971	CR257971 Forward s
28	163	4.2	751	25	AG606312	AG606312 Mus muscu
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c 31	162.4	4.2	958	5	BQ938645	BQ938645 AGENCOURT
c 32	162	4.2	457	7	CJ160607	CJ160607 CJ160607
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c 38	159	4.1	535	26	EF948816	EF948816 Mus muscu
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41	159	4.1	800	26	CR204927	CR204927 Reverse s
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ALIGNMENTS

RESULT 1

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 VERSION AZ660697.1 GI:11797843
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0538 row: K column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 649.

FEATURES

source	Location/Qualifiers
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ORIGIN

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Qy 1109 GAAACTACCATA TCAGGGCTAGAGAGATGGCTCAGCGGTTAACAGACTGACTGCTCTTC 1168
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 Db 421 AGAGCAACCAGAGGT CCTGTATTCAATTCCCAGCA ACCACATGATGGCTCACACCTGTA 480

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RESULT 2

AZ304757

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 clone UUGC1M0004O24 R, genomic survey sequence.
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 VERSION AZ304757.1 GI:10341090
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 High quality sequence stop: 589.
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnarecs/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptored DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number